



FASTA searches a protein or DNA sequence data bank
version 3.3t04 March 30, 2000
Please CITE
W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaCAaygaWej: 995 aa
>SEQ ID NO:2
vs /tmp/fastaDAAzgaWej library
searching /tmp/fastaDAAzgaWej library

1008 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2
join: 39, opt: 27, gap-pen: -12/-2, width: 16
Scan time: 0.034
The best scores are: opt
M13699 ACCESSION:M13699 NID: gi 180255 gb M13699. (1008) 2671

>>M13699 ACCESSION:M13699 NID: gi 180255 gb M13699.1 HUM (1008 aa)
initn: 1414 initl: 972 opt: 2671
Smith-Waterman score: 3980; 57.002% identity in 1014 aa overlap (1-992:1-1008)

	10	20	30	40	50	
SEQ	MKILILGIFLFLCSPGWAIDRHCIYIGIEESIWNYPSPGKNMLNEKPFSEDLE----					FLQ

M13699	MKILILGIFLFLCSTPAWAKEKHYYIGIETTWDYA----					SDHGEKKLISVDTEHSNIYQLQ
	10	20	30	40	50	
	60	70	80	90	100	110
SEQ	GGQARKSFVFKKALYFYTDNTFQRIIEKPSWLGFLGPMIKAETGDFIYVHVKNNASRAY					

M13699	NGPDRIGRLYKKALYLQYTDDETFRTTIEKPVWLGLGPIIKAETGDKVYVHLKNLASRPY					
	60	70	80	90	100	110
	120	130	140	150	160	170
SEQ	SYHPHGLTYSKENEAHGAIYPDNTTGLQKEVEYLEPGKQYTYKQYVEEHQGGPNDNSNCV					

M13699	TFHSHGITYYKEHE--GAIYPDNTTDFQRADDKVYPGEQYTYMLLATEEQSPGEGDGNCV					
	120	130	140	150	160	170
	180	190	200	210	220	230
SEQ	TRIIYSHIDTARDVASGLIGPILTKRGTLNGDTEKDIDRSSFLMFSTTDESRSWYSDEN					

M13699	TRIIYSHIDAPKDIASGLIGPLIICKKDSLDKEKEKHIDREFVVMFSVVDENFSWYLEDN					
	180	190	200	210	220	230
	240	250	260	270	280	290
SEQ	IRAF-TESGKINTSDPRFEESMSMQSINGYIYGNLPLNLTMCAEDRVQWYFVGMGGVADIH					

M13699	IKTYCSEPEKVDKDNEDFQESNRMYSVNGYTFGSLPGLSMCAEDRVKWLFGMGNEVDVH					
	240	250	260	270	280	290
	300	310	320	330	340	350
SEQ	PVYLRGQTLISRNRKDTIMLFPSSLEDAFMVAKAPGVWMLGCQ----					IHESMQAFFKVS

M13699	AAFFHGQALTNKNYRIDTINLFPATLFDAYMVAQNPGEWMLSCQNLNHLKAGLQAFFQVQ					
	300	310	320	330	340	350

	360	370	380	390	400	410
SEQ	NCQKPST	EAFVTG	THVIHY	YIAAKE	ILWNYA	PSGIDF
	:	:	:	:
M13699	ECNKSS	KDNIRG	KHVRHY	YIAAEE	IWNYAP	SGIDIF
	360	370	380	390	400	410

	420	430	440	450	460
SEQ	IGGTYK	KLIYRE	YTDASF	QTQKAR	---EEH
	:	:	:
M13699	IGGSYK	KLVIYR	EYTDAS	FTNRKE	RGPEEE
	420	430	440	450	460

	470	480	490	500	510	520
SEQ	QPPGLH	YNKSNE	GLFYE	---TPG	G-STPP	SSHVSP
	:	:	:	:
M13699	EPIGVR	FNKNNE	GTYYS	PNYNPQ	SRSVPP	SASHVA
	480	490	500	510	520	530

	530	540	550	560	570	580
SEQ	TWFYY	SSVNGK	KDINSG	LLGLLI	CRNGSL	GDDGKQ
	:	:	:	:
M13699	AKMYSA	VDPTKD	IFTGLI	GPMKIC	KKGSLH	ANGRQK
	540	550	560	570	580	590

	590	600	610	620	630	640
SEQ	N-RTFI	TEPENI	DKEDTD	CQASNK	MYSSIN	GMYGNL
	:	:	:	:	:	:
M13699	NIRMF	TTAPDQ	VDKEDE	DFQESN	KMHSMN	GFMYGN
	600	610	620	630	640	650

	650	660	670	680	690	700
SEQ	HGIYFS	GNTFTS	LGARRD	TIPMPY	TSQTLL	MTPDSI
	:	:	:	:	:
M13699	HGIYFS	GNTYLW	RGERRD	TANLFP	QTSLLH	MWPDTE
	660	670	680	690	700	710

	710	720	730	740	750	760
SEQ	RQCGKP	NPDPQT	OYQEEK	IIITIA	AEMEWD	YSPSRK
	::	:	:	:	:	:
M13699	NQCR	RQSE	DSTFYL	GERTYY	-IAAVE	VEWDYS
	720	730	740	750	760	770

	770	780	790	800	810	820
SEQ	LGSKYK	KVLYRQ	YDDNTF	TNQTKR	NEGEKH	LDILGP
	:	:	:	:	:
M13699	IGSKYK	KVVYRQ	YTDSTF	RVPPER	KAEEEH	LGI
	780	790	800	810	820	830

	830	840	850	860	870	880
SEQ	HAHGVK	TNNSTV	VP	TPQGEI	QIYT	WQIPDR
	:	:	:	:	:
M13699	HAHGVQ	TESSTV	TP	PLPGET	LT	YVWKIP
	840	850	860	870	880	890

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      890      900      910      920      930
SEQ    GPLSVCR----KDINPN-IVHRVLHFMIFDENESWYFEDSINTYASKPNKVDKENDNFQL
      :::  :::  :  :::  ..  .:  .....
M13699 GPLIVCRRPYLKVFNPRRKLEFALLFLVFDENESWYLDNKTYS DHPEKVNKDDEEFIE
      900      910      920      930      940      950

      940      950      960      970      980      990
SEQ    SNQMHAINGRLFGNNQGITFHVGDVVNWYLIGIGNEADLHTVHFHGH SFYKHKYLI
      .....: .....: .....: .....: .....: .....
M13699 SNKMHAINGRMFGNLQGLTMHVGDEVNWYLMGMGNEIDLHTVHFHGH SFQYKHR
      960      970      980      990      1000

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995 residues in 1 query sequences

1008 residues in 1 library sequences

Scomplib [version 3.3t05 March 30, 2000]

start: Wed Sep 18 11:18:07 2002 done: Wed Sep 18 11:18:08 2002

Scan time: 0.034 Display time: 1.433

Function used was FASTA